

# CONSERVATION GENOMICS OF THE ATLANTIC SALMON

*(Salmo salar)*

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Biosciences | Genetics Degree

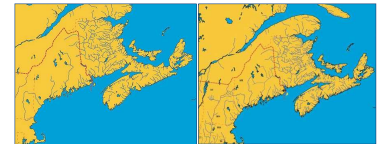


## INTRODUCTION

The loss of biodiversity is managed by Conservation Programs. Over the past years, Conservation Genomics has gained popularity, since it can shed some light on the mechanisms underlying local adaptation, as well as detect and predict introgression effects. Hence, it is an excellent tool for preserving species biodiversity.

North American Atlantic salmon populations have declined to an alarmingly low level during the past century, reaching the 16% of the original population, mainly because of habitat destruction, and now can only be found in very few rivers of Maine, USA, and of the Bay of Fundy, in the north-eastern Canadian coast.

For many years North American Atlantic salmon has been subject of Conservation efforts. Conservation Genomics can be crucial to the success of Conservation Programs, helping to preserve the Atlantic salmon biodiversity.



Comparison of current (left) and historical (right) habitat in the North East American coast. (atlanticsalmonfederation.org)

## GOALS AND METHODOLOGY

A review has been written to try to answer the questions:

- What is the current situation of Conservation Genomics in the Atlantic salmon conservation efforts?
- Is Conservation Genomics a useful tool in the conservation of the Atlantic salmon biodiversity?

## RESULTS

### SEQUENCING PROJECT

A sequencing project to publish the Atlantic salmon genome is in the works, and is managed by ICSASG (*International Collaboration to Sequence the Atlantic Salmon Genome*).

The final sequence has not been published yet, but a genome draft is available (NCBI Assembly ASM23337v1). Almost 34.000 genes have been identified, and it is estimated that repetitive DNA accounts for 35% of the Atlantic salmon genome, which has an haploid size of approximately  $3 \times 10^9$ bp.

The Atlantic salmon genome sequence will act as a reference sequence for salmonids.

### QTL ANALYSIS

Quantitative Trait Loci (QTLs) analysis can link phenotypic and genomic data to understand the genetic architecture of complex traits. Many of the QTLs that have been identified in Atlantic salmon are of traits related to survival:

Infectious Salmon Anemia: This disease causes high mortality in the Atlantic salmon population. The analysis of a QTL in chromosome 15 that gives resistance to ISA will help to reduce its incidence, and therefore, increase the likelihood of survival.



Li et al., 2011

Time of Emergency: the moment when the fry (young salmon) starts exogenous feeding is highly correlated to its chance of survival. 15 QTLs have been identified related to this trait. Considering the high mortality rates caused by migration, being able to identify QTLs that increase survival rate is key to maintain a population's integrity.

Number and contrast of skin marks: related to the ability of avoiding predators, at least three QTLs are responsible for the phenotypic variance of this trait.

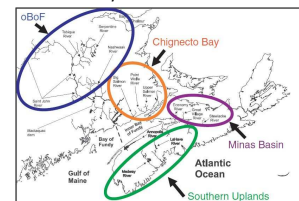
LG <sup>a</sup>	Trait <sup>b</sup>	pos <sup>c</sup> (cM)	r <sup>d</sup>	Mean <sup>e</sup>	s.e. <sup>f</sup>	Additive <sup>g</sup>	Dominance <sup>h</sup>	PEV <sup>i</sup>
AS1	asn(contrast)	0	8.17*	0.886	0.00572	-0.0232	0.0046	6.6
AS18	asn(num)	4	8.54*	1.006	0.00728	-0.0291	0.0133	6.8
AS19_31	asn(num)	0	9.7*	1.007	0.00746	-0.0317	0.0135	7.8
AS22_24	asn(num)	1	13.03**	1.018	0.00717	-0.0365	0.0028	10.3
AS22_24	asn(contrast)	30	33.49**	0.911	0.00602	-0.0278	-0.0326	25.6

Boulding et al., 2008

### ARRAYS

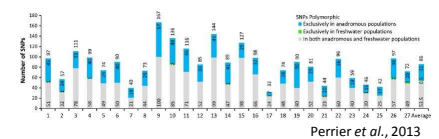
Arrays are becoming one of the most popular tools in Conservation Genomics, and they have been used to detect quantitative traits architecture, signs of selection and population structure.

Genetically distinct populations have been identified. High density arrays have been developed to study genetic differences between threatened populations, to establish Conservation Units and manage them with the minimum diversity loss.



Tymchuk et al., 2010

Through several studies with fine-scale arrays, Conservationists have been able to study adaptive divergence between anadromous and fresh water populations. Since the latter are more isolated, there is greater adaptive divergence among them.



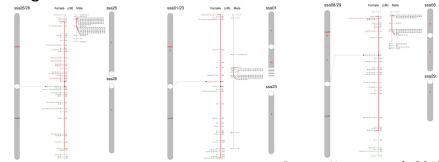
Perrier et al., 2013

Arrays have also been used to detect correlation between environment and genetic structure. Factors such as temperature and geology have been proved to be directly related to local adaptation and therefore, have to be considered when managing a population.

### COMPARATIVE GENOMICS

North American and European Atlantic salmon have different chromosome number ( $2n=58$  in Europe vs.  $2n=54$  chromosomes in North America). Though hybrids are viable, this is something to be considered in all Conservation Programs.

Comparative Genomics has been essential in the study of these chromosomal differences. By comparing linkage maps for both populations, it has been hypothesized that these changes were caused by three major events of reorganization.



Brenna-Hansen et al., 2012

## CONCLUSIONS

- The Atlantic salmon has many genetically distinct populations. The identification of genetic and environmental factors involved in **local adaptation** is an important step to establish Conservation Units and prevent biodiversity loss. Because of the complexity of this process, Genomic techniques become necessary.
- The main problem that threatens wild populations is farmed escapees. Wild and farmed Atlantic salmon have differences in their reproductive success, which translates in a lower fitness in hybrids. The final goal is to develop Genomic techniques to identify **introgression** signs as soon as possible to act accordingly.
- Conservation Genomics has been proved vital in the correct management of threatened Atlantic salmon populations. Though it is a relatively new specialization, it has quickly become an **essential part of the Atlantic salmon Conservation Programs**.
- Species conservation should be a **joint effort**. It is necessary to raise awareness of the importance of biodiversity, because extinction is a non reversible process.

## REFERENCES

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